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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/668,650

DATE: 06/27/2002
TIME: 14:02:04

Input Set : N:\Crf3\RULE60\09668650.raw
Output Set: N:\CRF3\06272002\I668650.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Bosch, Hendrick J.
6 Stiekema, Willem J.
8 (ii) TITLE OF INVENTION: Hybrid Toxin
10 (iii) NUMBER OF SEQUENCES: 15
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Novartis Corporation
14 (B) STREET: 3054 Cornwallis Road
15 (C) CITY: Research Triangle Park
16 (D) STATE: NC
17 (E) COUNTRY: USA
18 (F) ZIP: 27709
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US/09/668,650
28 (B) FILING DATE: 22-Sep-2000
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US/09/001,982
34 (B) FILING DATE:
36 (A) APPLICATION NUMBER: US 08/602,737
37 (B) FILING DATE: 21-FEB-1996
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Meigs, J. Timothy
41 (B) REGISTRATION NUMBER: 38,241
42 (C) REFERENCE/DOCKET NUMBER: 130-4080/PCT/CIP
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 919-541-8587
46 (B) TELEFAX: 919-541-8689

49 (2) INFORMATION FOR SEQ ID NO: 1:

- 51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 3567 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: unknown
57 (ii) MOLECULE TYPE: cDNA
59 (iii) HYPOTHETICAL: NO
C--> 61 (iv) ANTI-SENSE: NO

ENTERED

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63 (vi) ORIGINAL SOURCE:
64 (A) ORGANISM: Bacillus thuringiensis
66 (ix) FEATURE:
67 (A) NAME/KEY: CDS
68 (B) LOCATION: 1..3567
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT 48
74 Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
75 1 5 10 15
77 AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT 96
78 Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
79 20 25 30
81 TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC 144
82 Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
83 35 40 45
85 TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG 192
86 Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
87 50 55 60
89 GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA 240
90 Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
91 65 70 75 80
93 CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT 288
94 Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ile
95 85 90 95
97 GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA 336
98 Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
99 100 105 110
101 TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GAA ACC AGG ACC AGA 384
102 Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Glu Thr Arg Thr Arg
103 115 120 125
105 GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT 432
106 Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
107 130 135 140
109 CCT TCG TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT 480
110 Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
111 145 150 155 160
113 GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT 528
114 Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
115 165 170 175
117 TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT 576
118 Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
119 180 185 190
121 AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT 624
122 Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
123 195 200 205
125 ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT 672
126 Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
127 210 215 220
129 TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA 720

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130	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
131 225	230	235 240
133 GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT		768
134 Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile		
135 245	250	255
137 CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT		816
138 Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile		
139 260	265	270
141 AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC		864
142 Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn		
143 275	280	285
145 GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG		912
146 Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu		
147 290	295	300
149 AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT		960
150 Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe		
151 305	310	315 320
153 TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC		1008
154 Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Asn		
155 325	330	335
157 ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA		1056
158 Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg		
159 340	345	350
161 TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT		1104
162 Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr		
163 355	360	365
165 TTA CGA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT		1152
166 Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg		
167 370	375	380
169 GGT GTT GAA GGA GTA GAA TTT TCT ACA CCT ACA AAT AGC TTT ACG TAT		1200
170 Gly Val Glu Gly Val Glu Phe Ser Thr Pro Thr Asn Ser Phe Thr Tyr		
171 385	390	395 400
173 CGA GGA AGA GGT ACG GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT		1248
174 Arg Gly Arg Gly Thr Val Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp		
175 405	410	415
177 AAT AGT GTG CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA		1296
178 Asn Ser Val Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala		
179 420	425	430
181 ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT GGT GTA GTA		1344
182 Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr Gly Val Val		
183 435	440	445
185 TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT ACA AAT ACA ATT GAT CCA		1392
186 Phe Ser Trp Thr His Arg Ser Ala Thr Leu Thr Asn Thr Ile Asp Pro		
187 450	455	460
189 GAG AGA ATT AAT CAA ATA CCT TTA GTG AAA GGA TTT AGA GTT TGG GGG		1440
190 Glu Arg Ile Asn Gln Ile Pro Leu Val Lys Gly Phe Arg Val Trp Gly		
191 465	470	475 480
193 GGC ACC TCT GTC ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT		1488
194 Gly Thr Ser Val Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu		

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195	485	490	495	
197	CGA AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT ATT AAT			1536
198	Arg Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn Ile Asn			
199	500	505	510	
201	TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT CGT TAC GCT TCC AGT			1584
202	Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe Arg Tyr Ala Ser Ser			
203	515	520	525	
205	AGG GAT GCA CGA GTT ATA GTA TTA ACA GGA GCG GCA TCC ACA GGA GTG			1632
206	Arg Asp Ala Arg Val Ile Val Leu Thr Gly Ala Ala Ser Thr Gly Val			
207	530	535	540	
209	GGA GGC CAA GTT AGT GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA			1680
210	Gly Gly Gln Val Ser Val Asn Met Pro Leu Gln Lys Thr Met Glu Ile			
211	545	550	555	560
213	GGG GAG AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT AAT			1728
214	Gly Glu Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser Asn			
215	565	570	575	
217	CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG ATA AGT GAA CAA			1776
218	Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly Ile Ser Glu Gln			
219	580	585	590	
221	CCT CTA TTT GGT GCA GGT TCT ATT AGT AGC GGT GAA CTT TAT ATA GAT			1824
222	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp			
223	595	600	605	
225	AAA ATT GAA ATT ATT CTA GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT			1872
226	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp			
227	610	615	620	
229	TTA GAA AGA GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT			1920
230	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn			
231	625	630	635	640
233	CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT GAT CAA GTA			1968
234	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val			
235	645	650	655	
237	TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA TTT TGT CTG GAT GAA AAG			2016
238	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys			
239	660	665	670	
241	CGA GAA TTG TCC GAG AAA GTC AAA CAT GCG AAG CGA CTC AGT GAT GAG			2064
242	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu			
243	675	680	685	
245	CGG AAT TTA CTT CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA			2112
246	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro			
247	690	695	700	
249	GAC CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA GGA GAT			2160
250	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp			
251	705	710	715	720
253	GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG GGT ACC GTT GAT GAG			2208
254	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu			
255	725	730	735	
257	TGC TAT CCA ACG TAT TTA TAT CAG AAA ATA GAT GAG TCG AAA TTA AAA			2256
258	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys			
259	740	745	750	

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261	GCT TAT ACC CGT TAT GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC	2304
262	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp	
263	755 760 765	
265	TTA GAA ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT	2352
266	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn	
267	770 775 780	
269	GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC CAA AGT CCA ATC	2400
270	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile	
271	785 790 795 800	
273	GGA AAG TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT GAA TGG AAT	2448
274	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn	
275	805 810 815	
277	CCT GAT CTA GAT TGT TCC TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT	2496
278	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His	
279	820 825 830	
281	TCC CAT CAT TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT	2544
282	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn	
283	835 840 845	
285	GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC	2592
286	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly	
287	850 855 860	
289	CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA TTA TTA	2640
290	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro Leu Leu	
291	865 870 875 880	
293	GGG GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG AAG AAG TGG AGA GAC	2688
294	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp	
295	885 890 895	
297	AAA CGA GAG AAA CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA	2736
298	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala	
299	900 905 910	
301	AAA GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA	2784
302	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu	
303	915 920 925	
305	CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC GTT	2832
306	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val	
307	930 935 940	
309	CAT AGA ATC CGG GAA GCG TAT CTG CCA GAG TTG TCT GTG ATT CCA GGT	2880
310	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly	
311	945 950 955 960	
313	GTC AAT GCG GCC ATT TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG	2928
314	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala	
315	965 970 975	
317	TAT TCC TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC AAT	2976
318	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn	
319	980 985 990	
321	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
322	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
323	995 1000 1005	
325	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072

VERIFICATION SUMMARY DATE: 06/27/2002
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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:61 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:622 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1176 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1737 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]